



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/508,658
Source: 1655
Date Processed by STIC: 6/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/508,658

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 Use of <220> Sequence(s) 7-end of file missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1655

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/508,658

DATE: 06/21/2001

TIME: 11:43:24

Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

Does Not Comply
Corrected Diskette Needed

P. 6

```

3 <110> APPLICANT: Krohn, Kai
4      Heino, Maarit
5      Peterson, Part
6      Scott S., Hamish
7      Antonarakis E., Stylianos
8      Lalioti D., Maria
9      Shimizu, Nobuyoshi
10     Kudoh, Jun
12 <120> TITLE OF INVENTION: NOVEL GENE DEFECTIVE IN APECED AND ITS USE
14 <130> FILE REFERENCE: U0126539
16 <140> CURRENT APPLICATION NUMBER: 09/508,658
17 <141> CURRENT FILING DATE: 2000-11-03
19 <150> PRIOR APPLICATION NUMBER: PCT/FI98/00749
20 <151> PRIOR FILING DATE: 1998-09-23
22 <150> PRIOR APPLICATION NUMBER: 973762
23 <151> PRIOR FILING DATE: 1997-09-23
25 <160> NUMBER OF SEQ ID NOS: 36
27 <170> SOFTWARE: PatentIn Ver. 2.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2036
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
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36 <222> LOCATION: (137)..(1774)
37 <223> OTHER INFORMATION: /product="AIR-1"
39 <220> FEATURE:
40 <221> NAME/KEY: mat_peptide
41 <222> LOCATION: (1)..(545)
42 <223> OTHER INFORMATION: /product="AIR-1"
44 <400> SEQUENCE: 1
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47 cgaggccaag cgaggggctg ccagtgtccc gggaccacc gcgtccgcc cagccccggg 120
49 tccccgcgcc caccac atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg 172
50      Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg
51      1              5              10
53 ctg cac cgc acg gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg 220
54 Leu His Arg Thr Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu
55      15              20              25
57 ctg cac gcg ctg gct gac cac gac gtg gtc ccc gag gac aag ttt cag 268
58 Leu His Ala Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln
59      30              35              40
61 gag acg ctt cat ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac 316
62 Glu Thr Leu His Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His
63 45              50              55              60
65 gcc ctc ctg tcc tgg ctg ctg acc cag gac tcc aca gcc atc ctg gac 364
66 Ala Leu Leu Ser Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp

```

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Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

67		65		70		75	
69	ttc tgg agg gtg ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg						412
70	Phe Trp Arg Val Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg						
71		80		85		90	
73	ctg cag ccc atc ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag						460
74	Leu Gln Pro Ile Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln						
75		95		100		105	
77	ccc cgg aag ggg agg aag ccc ccg gcc gtc ccc aag gct ttg gta ccg						508
78	Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro						
79		110		115		120	
81	cca ccc aga ctc ccc acc aag agg aag gcc tca gaa gag gct cga gct						556
82	Pro Pro Arg Leu Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala						
83	125		130		135		140
85	gcc gcg cca gca gcc ctg act cca agg ggc acc gcc agc cca ggc tct						604
86	Ala Ala Pro Ala Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser						
87		145		150		155	
89	caa ctg aag gcc aag ccc ccc aag aag ccg gag agc agc gca gag cag						652
90	Gln Leu Lys Ala Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln						
91		160		165		170	
93	cag cgc ctt cca ctc ggg aac ggg att cag acc atg tca gct tca gtc						700
94	Gln Arg Leu Pro Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val						
95		175		180		185	
97	cag aga gct gtg gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg						748
98	Gln Arg Ala Val Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly						
99		190		195		200	
101	gcc gtg gag ggg atc ctc atc cag cag gtg ttt gag tca ggc ggc tcc						796
102	Ala Val Glu Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser						
103	205		210		215		220
105	aag aag tgc atc cag gtt ggc ggg gag ttc tac act ccc agc aag ttc						844
106	Lys Lys Cys Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe						
107		225		230		235	
109	gaa gac tcc ggc agt ggg aag aac aag gcc cgc agc agc agt ggc ccg						892
110	Glu Asp Ser Gly Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro						
111		240		245		250	
113	aag cct ctg gtt cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga						940
114	Lys Pro Leu Val Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly						
115		255		260		265	
117	ggt gag gct agg ctg ggc cag cag ggc agc gtt ccc gcc cct ctg gcc						988
118	Gly Glu Ala Arg Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala						
119		270		275		280	
121	ctc ccc agt gac ccc cag ctc cac cag aag aat gag gac gag tgt gcc						1036
122	Leu Pro Ser Asp Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala						
123	285		290		295		300
125	gtg tgt cgg gac ggc ggg gag ctc atc tgc tgt gac ggc tgc cct cgg						1084
126	Val Cys Arg Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg						
127		305		310		315	
129	gcc ttc cac ctg gcc tgc ctg tcc cct ccg ctc cgg gag atc ccc agt						1132
130	Ala Phe His Leu Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser						
131		320		325		330	

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Input Set : A:\U0126539.app

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```

133 ggg acc tgg agg tgc tcc agc tgc ctg cag gca aca gtc cag gag gtg 1180
134 Gly Thr Trp Arg Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val
135 335 340 345
137 cag ccc cgg gca gag gag ccc cgg cag gag cca ccc gtg gag acc 1228
138 Gln Pro Arg Ala Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr
139 350 355 360
141 ccg ctc ccc ccg ggg ctt agg tgc gcg gga gag gag gta aga ggt cca 1276
142 Pro Leu Pro Pro Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro
143 365 370 375 380
145 cct ggg gaa ccc cta gcc ggc atg gac acg act ctt gtc tac aag cac 1324
146 Pro Gly Glu Pro Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His
147 385 390 395
149 ctg ccg gct ccg cct tct gca gcc ccg ctg cca ggg ctg gac tcc tcg 1372
150 Leu Pro Ala Pro Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser
151 400 405 410
153 gcc ctg cac ccc cta ctg tgt gtg gct cct gag ggt cag cag aac ctg 1420
154 Ala Leu His Pro Leu Leu Cys Val Ala Pro Glu Gly Gln Gln Asn Leu
155 415 420 425
157 gct cct ggt gcg cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg 1468
158 Ala Pro Gly Ala Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu
159 430 435 440
161 cgg tgt act cac tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca 1516
162 Arg Cys Thr His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro
163 445 450 455 460
165 gcc ggc acc tcc cgg ccc ggg acg ggc ctg cgc tgc aga tcc tgc tca 1564
166 Ala Gly Thr Ser Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser
167 465 470 475
169 gga gac gtg acc cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc 1612
170 Gly Asp Val Thr Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro
171 480 485 490
173 gcc cgc ctg gcc cct ggg cct gcc aag gat gac act gcc agt cac gag 1660
174 Ala Arg Leu Ala Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu
175 495 500 505
177 ccc gct ctg cac agg gat gac ctg gag tcc ctt ctg agc gag cac acc 1708
178 Pro Ala Leu His Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr
179 510 515 520
181 ttc gat ggc atc ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg 1756
182 Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala
183 525 530 535 540
185 gcc ccc ttc ccc tcc tga cccagatgg ccgggacatg cagctctgat 1804
186 Ala Pro Phe Pro Ser
187 545
189 gagagagtgc tgagaaggac acctccttcc tcaagtctgg aagccggccg gctgggatca 1864
191 agaaggggac agcgccacct cttgtcagtg ctgggctgta aacagctctg tgtttctggg 1924
193 gacaccagcc atcatgtgcc tggaatttaa accctgcccc acttctctac tctggaagtc 1984
195 cccgggagcc tctccttgcc tggtagccta ctaaaaatat aaaaattagc tg 2036
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 545
200 <212> TYPE: PRT

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Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

201 <213> ORGANISM: Homo sapiens

203 <400> SEQUENCE: 2

```

204 Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
205      1      5      10      15
207 Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
208      20      25      30
210 Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
211      35      40      45
213 Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
214      50      55      60
216 Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
217      65      70      75      80
219 Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
220      85      90      95
222 Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
223      100     105     110
225 Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
226      115     120     125
228 Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Pro Ala
229      130     135     140
231 Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
232 145      150     155     160
234 Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
235      165     170     175
237 Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
238      180     185     190
240 Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
241      195     200     205
243 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
244      210     215     220
246 Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
247 225      230     235     240
249 Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
250      245     250     255
252 Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
253      260     265     270
255 Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
256      275     280     285
258 Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
259      290     295     300
261 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
262 305      310     315     320
264 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
265      325     330     335
267 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
268      340     345     350
270 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
271      355     360     365
273 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro

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RAW SEQUENCE LISTING

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Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

```

274      370      375      380
276 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
277 385      390      395      400
279 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
280      405      410      415
282 Leu Leu Cys Val Ala Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
283      420      425      430
285 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
286      435      440      445
288 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
289      450      455      460
291 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
292 465      470      475      480
294 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
295      485      490      495
297 Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
298      500      505      510
300 Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
301      515      520      525
303 Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
304      530      535      540
306 Ser
307 545
310 <210> SEQ ID NO: 3
311 <211> LENGTH: 1545
312 <212> TYPE: DNA
313 <213> ORGANISM: Homo sapiens
315 <220> FEATURE:
316 <221> NAME/KEY: CDS
317 <222> LOCATION: (237)..(1283)
318 <223> OTHER INFORMATION: /product="AIR-2"
320 <220> FEATURE:
321 <221> NAME/KEY: mat_peptide
322 <222> LOCATION: (1)..(348)
323 <223> OTHER INFORMATION: /product="AIR-2"
325 <400> SEQUENCE: 3
326 agagaaagtg aggtcttctc aggctcttaa gagcatggcg tttggtccag gctgtaccgg 60
328 ctgctctcag ctgggcccggt ggggtggccg ggcgcctctg ctatagccag gaggtcaagg 120
330 atccactggg aatgccatgc tcattcttcg tccccagcat ggtttcttaa tggggtagaa 180
332 gcaggtcggg agagacctcc ctgggcctgg cccactgcc ctgtgaggaa gggttc atg 239
333 Met
334 1
336 tgg ttg gtg tac agt tcc ggg gcc cct gga acg cag cag cct gca aga 287
337 Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala Arg
338      5      10      15
340 aac cgg gtt ttc ttc cca ata ggg atg gcc ccg ggg ggt gtc tgt tcg 335
341 Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys Ser
342      20      25      30
344 aga cca gat gga tgg gga aca ggt ggt cag ggc aga att tca ggc cct 383

```

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

See item 11 on Error Summary Sheet

<400> 7
 gatgacactg ccagtcacga

20

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<400> 8
 gttcccaggt ggaaggcgct gc

22

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<400> 9
 aggggacagg caggccaggt

20

The above sequences are samples of global errors.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

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Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

L:596 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
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L:675 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:684 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:684 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:693 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:693 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:702 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:702 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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PATENT APPLICATION: US/09/508,658

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Input Set : A:\U0126539.app

Output Set: N:\CRF3\06202001\I508658.raw

L:923 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:932 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:932 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: